

## SEQUENCE LISTING

&lt;110&gt; NOVO NORDISK A/S

&lt;120&gt; NOVEL MANNANASES

&lt;130&gt; 5440-WO

&lt;140&gt;

&lt;141&gt;

&lt;160&gt; 34

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1470

&lt;212&gt; DNA

&lt;213&gt; Bacillus sp. I633

&lt;400&gt; 1

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&lt;210&gt; 2

&lt;211&gt; 490

&lt;212&gt; PRT

&lt;213&gt; Bacillus sp. I633

&lt;400&gt; 2

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  1                      5                      10                      15

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Leu Ala Ser Ser Ile Leu Phe Val Ser Gly Thr Ser Thr Ala Asn Ala
      20                      25                      30

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Asn Ser Gly Phe Tyr Val Ser Gly Thr Thr Leu Tyr Asp Ala Asn Gly  
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 Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys  
 50 55 60  
 Asp Gln Ala Thr Thr Ala Ile Glu Gly Ile Ala Asn Thr Gly Ala Asn  
 65 70 75 80  
 Thr Val Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Thr Lys Asp Asp  
 85 90 95  
 Ile His Thr Val Arg Asn Leu Ile Ser Leu Ala Glu Asp Asn His Leu  
 100 105 110  
 Val Ala Val Pro Glu Val His Asp Ala Thr Gly Tyr Asp Ser Ile Ala  
 115 120 125  
 Ser Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Arg Ser Ala Leu  
 130 135 140  
 Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Phe  
 145 150 155 160  
 Gly Ser Trp Glu Gly Asp Ala Trp Ala Asp Gly Tyr Lys Gln Ala Ile  
 165 170 175  
 Pro Arg Leu Arg Asn Ala Gly Leu Asn His Thr Leu Met Val Asp Ala  
 180 185 190  
 Ala Gly Trp Gly Gln Phe Pro Gln Ser Ile His Asp Tyr Gly Arg Glu  
 195 200 205  
 Val Phe Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Ile His Met  
 210 215 220  
 Tyr Glu Tyr Ala Gly Gly Asn Ala Ser Gln Val Arg Thr Asn Ile Asp  
 225 230 235 240  
 Arg Val Leu Asn Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His  
 245 250 255  
 Arg His Thr Asn Gly Asp Val Asp Glu Ala Thr Ile Met Ser Tyr Ser  
 260 265 270  
 Glu Gln Arg Gly Val Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Gly  
 275 280 285  
 Pro Glu Trp Glu Tyr Leu Asp Leu Ser Asn Asp Trp Ala Gly Asn Asn  
 290 295 300  
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 305 310 315 320  
 Glu Thr Ser Arg Leu Ser Thr Val Phe Thr Gly Gly Gly Ser Asp Gly  
 325 330 335  
 Gly Thr Ser Pro Thr Thr Leu Tyr Asp Phe Glu Gly Ser Met Gln Gly  
 340 345 350

Trp Thr Gly Ser Ser Leu Ser Gly Gly Pro Trp Ala Val Thr Glu Trp  
355 360 365

Ser Ser Lys Gly Ser His Ser Leu Lys Ala Asp Ile Gln Leu Ser Ser  
370 375 380

Asn Ser Gln His Tyr Leu His Val Ile Gln Asn Thr Ser Leu Gln Gln  
385 390 395 400

Asn Ser Arg Ile Gln Ala Thr Val Lys His Ala Asn Trp Gly Ser Val  
405 410 415

Gly Asn Gly Met Thr Ala Arg Leu Tyr Val Lys Thr Gly His Gly Tyr  
420 425 430

Thr Trp Tyr Ser Gly Ser Phe Val Pro Ile Asn Gly Ser Ser Gly Thr  
435 440 445

Thr Leu Ser Leu Asp Leu Ser Asn Val Gln Asn Leu Ser Gln Val Arg  
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Ser Ile Tyr Ile Asp Asn Val Ile Val Glu  
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<210> 3

<211> 1438

<212> DNA

<213> Bacillus sp. I633

<400> 3

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tataaacaag caatcccgcg attgcgtaac gccggtctaa accatacctt gatggttagat 480
gctgcggggt ggggacaatt tccacaatcg attcatgatt atggaagaga agtttttaat 540
gctgaccctc aacgaaatac aatgttttcg attcatatgt atgaatatgc aggtggtaat 600
gcatcgcaag ttcgtactaa tattgaccga gttcttaatc aagacctcgc attagtcatt 660
ggtgaatttg gacaccgtca taaaaatggt gacgtcgatg aagcaacgat tatgagctat 720
tctgaacaaa gaggagttag gtggttggtg tggtcatgga aagggaaacgg ccagaaatgg 780
gagtatttag acctttcgaa tgattgggct ggaaataacc ttacagcttg gggaaataca 840
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gtagacggac agaaagatca gaccttctgg tgtgaccatg ctgcaataat cggcagtaac 1140
ggcagctaca acggaattac ttcaaatgta aaaggaacat ttgtaaaaat gagttcctca 1200
acaaataacg cagacaccta ccttgaaata agctttacag gcggaactct tgaaccgggt 1260
gcacatgttc agatacaagg tagatttgca aagaatgact ggagtaacta tacacagtca 1320
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<210> 4  
 <211> 476  
 <212> PRT  
 <213> Bacillus sp.

<400> 4

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Lys	Asp	Gln	Ala	Thr	Thr	Ala	Ile	Glu	Gly	Ile	Ala	Asn	Thr	Gly	Ala	35	40	45	
Asn	Thr	Val	Arg	Ile	Val	Leu	Ser	Asp	Gly	Gly	Gln	Trp	Thr	Lys	Asp	50	55	60	
Asp	Ile	His	Thr	Val	Arg	Asn	Leu	Ile	Ser	Leu	Ala	Glu	Asp	Asn	His	65	70	75	80
Leu	Val	Ala	Val	Pro	Glu	Val	His	Asp	Ala	Thr	Gly	Tyr	Asp	Ser	Ile	85	90	95	
Ala	Ser	Leu	Asn	Arg	Ala	Val	Asp	Tyr	Trp	Ile	Glu	Met	Arg	Ser	Ala	100	105	110	
Leu	Ile	Gly	Lys	Glu	Asp	Thr	Val	Ile	Ile	Asn	Ile	Ala	Asn	Glu	Trp	115	120	125	
Phe	Gly	Ser	Trp	Glu	Gly	Asp	Ala	Trp	Ala	Asp	Gly	Tyr	Lys	Gln	Ala	130	135	140	
Ile	Pro	Arg	Leu	Arg	Asn	Ala	Gly	Leu	Asn	His	Thr	Leu	Met	Val	Asp	145	150	155	160
Ala	Ala	Gly	Trp	Gly	Gln	Phe	Pro	Gln	Ser	Ile	His	Asp	Tyr	Gly	Arg	165	170	175	
Glu	Val	Phe	Asn	Ala	Asp	Pro	Gln	Arg	Asn	Thr	Met	Phe	Ser	Ile	His	180	185	190	
Met	Tyr	Glu	Tyr	Ala	Gly	Gly	Asn	Ala	Ser	Gln	Val	Arg	Thr	Asn	Ile	195	200	205	
Asp	Arg	Val	Leu	Asn	Gln	Asp	Leu	Ala	Leu	Val	Ile	Gly	Glu	Phe	Gly	210	215	220	
His	Arg	His	Thr	Asn	Gly	Asp	Val	Asp	Glu	Ala	Thr	Ile	Met	Ser	Tyr	225	230	235	240
Ser	Glu	Gln	Arg	Gly	Val	Gly	Trp	Leu	Ala	Trp	Ser	Trp	Lys	Gly	Asn	245	250	255	
Gly	Pro	Glu	Trp	Glu	Tyr	Leu	Asp	Leu	Ser	Asn	Asp	Trp	Ala	Gly	Asn	260	265	270	
Asn	Leu	Thr	Ala	Trp	Gly	Asn	Thr	Ile	Val	Asn	Gly	Pro	Tyr	Gly	Leu	275	280	285	

Arg Glu Thr Ser Arg Leu Ser Thr Val Phe Thr Ala Ser Pro Glu Pro  
 290 295 300  
 Thr Pro Glu Pro Thr Ala Asn Thr Pro Val Ser Gly Asn Leu Lys Val  
 305 310 315 320  
 Glu Phe Tyr Asn Ser Asn Pro Ser Asp Thr Thr Asn Ser Ile Asn Pro  
 325 330 335  
 Gln Phe Lys Val Thr Asn Thr Gly Ser Ser Ala Ile Asp Leu Ser Lys  
 340 345 350  
 Leu Thr Leu Arg Tyr Tyr Tyr Thr Val Asp Gly Gln Lys Asp Gln Thr  
 355 360 365  
 Phe Trp Cys Asp His Ala Ala Ile Ile Gly Ser Asn Gly Ser Tyr Asn  
 370 375 380  
 Gly Ile Thr Ser Asn Val Lys Gly Thr Phe Val Lys Met Ser Ser Ser  
 385 390 395 400  
 Thr Asn Asn Ala Asp Thr Tyr Leu Glu Ile Ser Phe Thr Gly Gly Thr  
 405 410 415  
 Leu Glu Pro Gly Ala His Val Gln Ile Gln Gly Arg Phe Ala Lys Asn  
 420 425 430  
 Asp Trp Ser Asn Tyr Thr Gln Ser Asn Asp Tyr Ser Phe Lys Ser Arg  
 435 440 445  
 Ser Gln Phe Val Glu Trp Asp Gln Val Thr Ala Tyr Leu Asn Gly Val  
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 Leu Val Trp Gly Lys Glu Pro Gly Gly Ser Val Val  
 465 470 475

<210> 5

<211> 1482

<212> DNA

<213> Bacillus agaradhaerens

<400> 5

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 aatacgttat atgacgcaaa tgggcagcca tttgtcatga gaggtattaa ccatggacat 180  
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 cgtgaagtca ttgagcttgc ggagcaaaat aaaatgggtg ctgtcggtga agttcatgat 360  
 gccacgggtc gcgattcgcg cagtgattta aatcgagccg ttgattattg gatagaaatg 420  
 aaagatgcgc ttatcggtaa agaagatacg gttattatta acattgcaaa cgagtgggat 480  
 gggagttggg atggctcagc ttgggcgat ggctatattg atgtcattcc gaagcttcgc 540  
 gatgccggct taacacacac cttaatgggt gatgcagcag gatgggggca atatccgcaa 600  
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 tccatccata tgtatgagta tgctggtggt gatgctaaca ctggttagatc aaatattgat 720  
 agagtcatag atcaagacct tgctctcgta ataggtgaat tcggtcatag acatactgat 780  
 ggtgatgttg atgaagatac aatccttagt tattctgaag aaactggcac aggggtggctc 840  
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<210> 6
<211> 493
<212> PRT
<213> Bacillus agaradhaerens
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      20           25           30
Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly
      35           40           45
Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
      50           55           60
Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn
  65           70           75           80
Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp
      85           90           95
Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met
      100           105           110
Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser
      115           120           125
Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu
      130           135           140
Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr
  145           150           155           160
Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile
      165           170           175
Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala
      180           185           190
Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp
      195           200           205
Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met
      210           215           220

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Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp  
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 Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His  
 245 250 255  
 Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser  
 260 265 270  
 Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser  
 275 280 285  
 Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His  
 290 295 300  
 Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln  
 305 310 315 320  
 Glu Thr Ser Lys Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His  
 325 330 335  
 Pro Glu Pro Pro Thr Ala Thr Thr Leu Tyr Asp Phe Glu Gly Ser Thr  
 340 345 350  
 Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr  
 355 360 365  
 Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu  
 370 375 380  
 Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu  
 385 390 395 400  
 His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly  
 405 410 415  
 Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser  
 420 425 430  
 Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn  
 435 440 445  
 Ser Gly Thr Thr Leu Ser Phe Asp Leu Asn Asn Ile Glu Asn Ser His  
 450 455 460  
 His Val Arg Glu Ile Gly Val Gln Phe Ser Ala Ala Asp Asn Ser Ser  
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 Gly Gln Thr Ala Leu Tyr Val Asp Asn Val Thr Leu Arg  
 485 490

<210> 7

<211> 1407

<212> DNA

<213> Bacillus agaradhaerens

<400> 7

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aatacgttat atgacgcaaa tgggcagcca tttgtcatga gaggtattaa ccatggacat 180
gcttggtata aagacaccgc ttcaacagct attcctgcca ttgcagagca aggcgccaac 240
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cgtgaagtca ttgagcttgc ggagcaaaat aaaatgggtg ctgtcgttga agttcatgat 360
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<210> 8

<211> 468

<212> PRT

<213> *Bacillus agaradhaerens*

<400> 8

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      20              25              30

Ser Thr Gly Phe Tyr Val Asp Gly Asn Thr Leu Tyr Asp Ala Asn Gly
      35              40              45

Gln Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Tyr Lys
      50              55              60

Asp Thr Ala Ser Thr Ala Ile Pro Ala Ile Ala Glu Gln Gly Ala Asn
      65              70              75              80

Thr Ile Arg Ile Val Leu Ser Asp Gly Gly Gln Trp Glu Lys Asp Asp
      85              90              95

Ile Asp Thr Ile Arg Glu Val Ile Glu Leu Ala Glu Gln Asn Lys Met
      100              105              110

Val Ala Val Val Glu Val His Asp Ala Thr Gly Arg Asp Ser Arg Ser
      115              120              125

Asp Leu Asn Arg Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Ala Leu
      130              135              140

Ile Gly Lys Glu Asp Thr Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr
      145              150              155              160

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Gly Ser Trp Asp Gly Ser Ala Trp Ala Asp Gly Tyr Ile Asp Val Ile  
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 Pro Lys Leu Arg Asp Ala Gly Leu Thr His Thr Leu Met Val Asp Ala  
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 Ala Gly Trp Gly Gln Tyr Pro Gln Ser Ile His Asp Tyr Gly Gln Asp  
 195 200 205  
 Val Phe Asn Ala Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met  
 210 215 220  
 Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Ser Asn Ile Asp  
 225 230 235 240  
 Arg Val Ile Asp Gln Asp Leu Ala Leu Val Ile Gly Glu Phe Gly His  
 245 250 255  
 Arg His Thr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr Ser  
 260 265 270  
 Glu Glu Thr Gly Thr Gly Trp Leu Ala Trp Ser Trp Lys Gly Asn Ser  
 275 280 285  
 Thr Glu Trp Asp Tyr Leu Asp Leu Ser Glu Asp Trp Ala Gly Gln His  
 290 295 300  
 Leu Thr Asp Trp Gly Asn Arg Ile Val His Gly Ala Asp Gly Leu Gln  
 305 310 315 320  
 Glu Thr Ser Lys Pro Ser Thr Val Phe Thr Asp Asp Asn Gly Gly His  
 325 330 335  
 Pro Glu Pro Pro Thr Ala Thr Thr Leu Tyr Asp Phe Glu Gly Ser Thr  
 340 345 350  
 Gln Gly Trp His Gly Ser Asn Val Thr Gly Gly Pro Trp Ser Val Thr  
 355 360 365  
 Glu Trp Gly Ala Ser Gly Asn Tyr Ser Leu Lys Ala Asp Val Asn Leu  
 370 375 380  
 Thr Ser Asn Ser Ser His Glu Leu Tyr Ser Glu Gln Ser Arg Asn Leu  
 385 390 395 400  
 His Gly Tyr Ser Gln Leu Asn Ala Thr Val Arg His Ala Asn Trp Gly  
 405 410 415  
 Asn Pro Gly Asn Gly Met Asn Ala Arg Leu Tyr Val Lys Thr Gly Ser  
 420 425 430  
 Asp Tyr Thr Trp His Ser Gly Pro Phe Thr Arg Ile Asn Ser Ser Asn  
 435 440 445  
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 450 455 460  
 Met Leu Gly Lys  
 465

<210> 9  
 <211> 1761  
 <212> DNA  
 <213> *Bacillus halodurans*

<400> 9  
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 caaaacgcat ctcaatatac aaaagagttg tttgcctttt tacgtgatgt aagtggtaaa 180  
 caagttttat ttggtcaaca acacgcaact gatgagggtat taacacttag aggaacaggt 240  
 aaccgaattg gttcaacaga atcagaagtg aaaaatgctg ttggtgatta tcctgctggt 300  
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 caagaacaaa gaatcttaaa tacagcagct tcaatgaagg cagctcacga cttagggtggg 420  
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 actggaaatg ttgtacaaga aattcttcct ggtggatcaa agcatgaaga attcaatgca 540  
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 ccaattattt tccgtccttt ccatgagcaa acaggttctt ggttctgggt gggagcaagc 660  
 acaacaactc cagaacagta taaagctatt tacagatata cgggtgaata cttacgtgac 720  
 gtaaaaggag caaacaactt cttatagcgt ttttctcctg gtgcagggtcc agctggcgat 780  
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 gggtacagtg caacagggtat gaatcgtact ggtaacacat tggattggta tactcgttta 1020  
 cttaatgcaa taaaagaaga tccaaaagca agtaagattt cttacatgct tacatgggca 1080  
 aactttgggt tccctaacaa tatgtatggt ccttacaaag acattcacgg tgatttaggt 1140  
 ggagatcatg aactccttcc agatttcac ccaattttttg aagatgatta ctcagctttc 1200  
 acaggagata tcaagggaaa tgtgtatgat acaggaattg aatatactgt agcaccacat 1260  
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 ttacgagcta aagtattaaa cgatgataac gcagttgtta cgtacagggt tgaaggttct 1380  
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 <212> PRT  
 <213> *Bacillus halodurans*

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 Gly Gln Glu Leu Lys Met Thr Asp Gln Asn Ala Ser Gln Tyr Thr Lys  
 35 40 45  
 Glu Leu Phe Ala Phe Leu Arg Asp Val Ser Gly Lys Gln Val Leu Phe  
 50 55 60  
 Gly Gln Gln His Ala Thr Asp Glu Gly Leu Thr Leu Arg Gly Thr Gly

80

Category	Item	Value
Agriculture	Wheat	1000
	Corn	800
	Barley	600
	Oats	500
Manufacturing	Iron	1200
	Steel	1100
	Textiles	900
	Chemicals	700
Services	Transport	1500
	Finance	1300
	Health	1100
	Education	1000

385	390	395	400
Thr Gly Asp Ile Lys Gly Asn Val Tyr Asp Thr Gly Ile Glu Tyr Thr	405	410	415
Val Ala Pro His Glu Arg Leu Met Tyr Val Leu Ser Pro Ile Thr Gly	420	425	430
Thr Thr Ile Thr Asp Thr Val Thr Leu Arg Ala Lys Val Leu Asn Asp	435	440	445
Asp Asn Ala Val Val Thr Tyr Arg Val Glu Gly Ser Asp Val Glu His	450	455	460
Glu Met Thr Leu Ala Asp Ser Gly Tyr Tyr Thr Ala Lys Tyr Ser Pro	465	470	475
Thr Ala Glu Val Asn Gly Gly Ser Val Asp Leu Thr Val Thr Tyr Trp	485	490	495
Ser Gly Glu Glu Lys Val Gln Asp Glu Val Ile Arg Leu Tyr Val Lys	500	505	510
Ala Ser Glu Ile Ser Leu Tyr Lys Leu Thr Phe Asp Glu Asp Ile Asn	515	520	525
Gly Ile Lys Ser Asn Gly Thr Trp Pro Glu Asp Gly Ile Thr Ser Asp	530	535	540
Val Ser His Val Ser Phe Asp Gly Asn Gly Lys Leu Lys Phe Ala Val	545	550	555
Asn Gly Met Ser Ser Glu Glu Trp Trp Gln Glu Leu Lys Leu Glu Leu	565	570	575
Thr Asp Leu Ser Asp Val Asn Leu Ala Lys	580	585	

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 <211> 995  
 <212> DNA  
 <213> Bacillus sp. AAI12

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 ggtacaacat tatatgatgc aaatggaaac ccttttggtta tgagagggat taatcatgga 180  
 catgcttggt ttaaacaaga actagaaaca tccatgagag ggattagtca aacaggggca 240  
 aatacgattc gtgtcgtttt gtctaattggg caaagatggc aaaaagatga tcgaaacatg 300  
 gtagcttcgg ttatttcttt ggcagagcag catcaaataa ttgccgtttt agaagttcat 360  
 gatgctactg gtagcaataa tttctccgat ctgcaagctg ctgtggacta ttggattgag 420  
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 tacggtgctt gggacggagg cgcattgggca cgagggtatc agaatgcgat acgtcagctt 540  
 cgaaatgcag gcttgtcaca tacatttatg gttgacgctg ccggttatgg ccagtaccct 600  
 caatcggtag ttgattatgg tcaagaagta ttaaatgctg acccacagag aaacacaatg 660  
 ttttctgttc atatgtatga atatgcaggc ggagatgcta atacagtaag acgaaacatt 720  
 gactcgatct taagccagaa cttagctctt gtcattggtg aattcgggca ttggcattat 780  
 gacggtgatg ttgatgagga caccatttta agctattcac agcaaagaaa tgtgggatgg 840

ttggcgtgga gctggcatgg caatagtga ggggtcgaat atcttgattt atcgaatgac 900  
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 cgtcaaacct ctaaaagaag cagtgtgttt caata 995

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 Leu Ile Phe Ala Gly Val Leu Asn Thr Ser Ser Ser Gln Ala Glu Ala  
           20                  25                  30  
 His His Ser Gly Phe His Val Asn Gly Thr Thr Leu Tyr Asp Ala Asn  
           35                  40                  45  
 Gly Asn Pro Phe Val Met Arg Gly Ile Asn His Gly His Ala Trp Phe  
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 Lys Gln Glu Leu Glu Thr Ser Met Arg Gly Ile Ser Gln Thr Gly Ala  
           65                  70                  75                  80  
 Asn Thr Ile Arg Val Val Leu Ser Asn Gly Gln Arg Trp Gln Lys Asp  
                   85                  90                  95  
 Asp Arg Asn Met Val Ala Ser Val Ile Ser Leu Ala Glu Gln His Gln  
           100                  105                  110  
 Met Ile Ala Val Leu Glu Val His Asp Ala Thr Gly Ser Asn Asn Phe  
           115                  120                  125  
 Ser Asp Leu Gln Ala Ala Val Asp Tyr Trp Ile Glu Met Lys Asp Val  
           130                  135                  140  
 Leu Gln Gly Lys Glu Asp Ile Val Ile Ile Asn Ile Ala Asn Glu Trp  
           145                  150                  155                  160  
 Tyr Gly Ala Trp Asp Gly Gly Ala Trp Ala Arg Gly Tyr Gln Asn Ala  
                   165                  170                  175  
 Ile Arg Gln Leu Arg Asn Ala Gly Leu Ser His Thr Phe Met Val Asp  
                   180                  185                  190  
 Ala Ala Gly Tyr Gly Gln Tyr Pro Gln Ser Val Val Asp Tyr Gly Gln  
           195                  200                  205  
 Glu Val Leu Asn Ala Asp Pro Gln Arg Asn Thr Met Phe Ser Val His  
           210                  215                  220  
 Met Tyr Glu Tyr Ala Gly Gly Asp Ala Asn Thr Val Arg Arg Asn Ile  
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 Asp Ser Ile Leu Ser Gln Asn Leu Ala Leu Val Ile Gly Glu Phe Gly  
                   245                  250                  255  
 His Trp His Tyr Asp Gly Asp Val Asp Glu Asp Thr Ile Leu Ser Tyr

260

265

270

Ser Gln Gln Arg Asn Val Gly Trp Leu Ala Trp Ser Trp His Gly Asn  
275 280 285

Ser Glu Gly Val Glu Tyr Leu Asp Leu Ser Asn Asp Phe Ala Gly Asn  
290 295 300

Arg Leu Thr Trp Trp Gly Asp Arg Ile Val Asn Gly Pro Asn Gly Ile  
305 310 315 320

Arg Gln Thr Ser Lys Arg Ser Ser Val Phe Gln  
325 330

&lt;210&gt; 13

&lt;211&gt; 1464

&lt;212&gt; DNA

&lt;213&gt; Humicola insolens

&lt;400&gt; 13

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gttgagtcga gctcgccgg ctactctggt accggatatg tagcgggctt cgacgagccc 240
agtgacaaga tcacgttcca cgtggacagc gagaccacac ggctgtacga cctcaccatc 300
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attcaggggt ggaggaacgc gcaa 1464

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&lt;211&gt; 488

&lt;212&gt; PRT

&lt;213&gt; Humicola insolens

&lt;400&gt; 14

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Ser Gly Ala Val Ala Ala Pro Tyr Cys Ala Pro Gln Pro Ser Thr Thr  
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Ser Gln Glu Pro Thr Ser Thr Pro Ser Pro Val Pro Gly Pro Arg Thr  
 35 40 45  
 Phe Glu Ala Glu Asp Ala Ile Leu Thr Gly Thr Arg Val Glu Ser Ser  
 50 55 60  
 Leu Ala Gly Tyr Ser Gly Thr Gly Tyr Val Ala Gly Phe Asp Glu Pro  
 65 70 75 80  
 Ser Asp Lys Ile Thr Phe His Val Asp Ser Glu Thr Thr Arg Leu Tyr  
 85 90 95  
 Asp Leu Thr Ile Arg Val Ala Ala Ile Tyr Gly Glu Lys Arg Thr Thr  
 100 105 110  
 Val Val Leu Asn Asn Gly Ala Ala Ser Glu Val Tyr Phe Pro Ala Gly  
 115 120 125  
 Asp Ser Phe Val Asp Ile Ala Ala Gly Gln Val Leu Leu Asn Gln Gly  
 130 135 140  
 Asp Asn Thr Ile Asp Ile Val Asn Asn Trp Gly Trp Tyr Leu Ile Asp  
 145 150 155 160  
 Ser Ile Thr Ile Thr Pro Ser Ala Pro Arg Pro Pro His Gln Ile Asn  
 165 170 175  
 Pro Ser Pro Val Asn Pro Ala Ala Asp Asp Asn Ala Arg Ala Leu Tyr  
 180 185 190  
 Ala Tyr Leu Arg Ser Ile Tyr Gly Lys Lys Ile Leu Ser Gly Gln Gln  
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 Glu Leu Ser Trp Ala Asn Trp Ile Ala Gln Gln Thr Gly Lys Thr Pro  
 210 215 220  
 Ala Leu Val Ser Val Asp Met Met Asp Tyr Ser Pro Ser Arg Val Glu  
 225 230 235 240  
 Arg Gly Thr Val Gly Ser Ala Val Glu Glu Ala Ile Glu His His Arg  
 245 250 255  
 Arg Gly Gly Ile Val Ser Val Leu Trp His Trp Asn Ala Pro Thr Gly  
 260 265 270  
 Leu Tyr Asp Thr Pro Glu Arg Arg Trp Trp Ser Gly Phe Tyr Thr Asp  
 275 280 285  
 Ala Thr Asp Phe Asp Val Ala Arg Ala Leu Ala Asp Thr Thr Asn Ala  
 290 295 300  
 Asn Tyr Thr Leu Leu Ile Arg Asp Ile Asp Ala Ile Ala Val Gln Leu  
 305 310 315 320  
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 325 330 335  
 Glu Ala Glu Gly Gly Trp Phe Trp Trp Gly Ala Lys Gly Pro Glu Ala  
 340 345 350

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Tyr Lys Lys Leu Trp Gly Ile Leu Tyr Asp Arg Leu Thr Asn Tyr His  
355 360 365

Gly Leu Asn Asn Leu Leu Trp Val Trp Asn Ser Ile Leu Pro Glu Trp  
370 375 380

Tyr Pro Gly Asp Glu Thr Val Asp Ile Val Ser Ala Asp Val Tyr Ala  
385 390 395 400

Gln Gly Asn Gly Pro Met Ser Thr Gln Tyr Asn Gln Leu Ile Glu Leu  
405 410 415

Gly Lys Asp Lys Lys Met Ile Ala Ala Thr Glu Val Gly Ala Ala Pro  
420 425 430

Leu Pro Asp Leu Leu Gln Ala Tyr Glu Ala His Trp Leu Trp Phe Ala  
435 440 445

Val Trp Gly Asp Thr Phe Ile Asn Asn Pro Gln Trp Asn Ser Ile Glu  
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Thr Leu Lys Thr Ile Tyr Asn Ser Asp Tyr Val Leu Thr Leu Asp Glu  
465 470 475 480

Ile Gln Gly Trp Arg Asn Ala Gln  
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<212> DNA  
<213> Bacillus sp. AA349

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caagctgaag cacctggaaa aacggctgaa aatggagtct gggataaagt tcgaaataat 180  
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<210> 16  
<211> 369  
<212> PRT



&lt;213&gt; Bacillus sp. AA349

&lt;400&gt; 16

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Ser	Phe	Thr	Phe	Asn	Leu	Val	Val	Ala	Gln	Ala	Ser	Gly	His	Gly	Gln	20	25	30	
Met	His	Lys	Val	Pro	Trp	Ala	Pro	Gln	Ala	Glu	Ala	Pro	Gly	Lys	Thr	35	40	45	
Ala	Glu	Asn	Gly	Val	Trp	Asp	Lys	Val	Arg	Asn	Asn	Pro	Gly	Lys	Ala	50	55	60	
Asn	Pro	Pro	Ala	Gly	Lys	Val	Asn	Gly	Phe	Tyr	Ile	Asp	Gly	Thr	Thr	65	70	75	80
Leu	Tyr	Asp	Ala	Asn	Gly	Lys	Pro	Phe	Val	Met	Arg	Gly	Ile	Asn	His	85	90	95	
Gly	His	Ser	Trp	Tyr	Lys	Pro	His	Ile	Glu	Thr	Ala	Met	Glu	Ala	Ile	100	105	110	
Ala	Asp	Thr	Gly	Ala	Asn	Ser	Ile	Arg	Val	Val	Leu	Ser	Asp	Gly	Gln	115	120	125	
Gln	Trp	Thr	Lys	Asp	Asp	Val	Asp	Glu	Val	Ala	Lys	Ile	Ile	Ser	Leu	130	135	140	
Ala	Glu	Lys	His	Ser	Leu	Val	Ala	Ala	Leu	Glu	Val	His	Asp	Ala	Leu	145	150	155	160
Gly	Thr	Asp	Asp	Ile	Glu	Pro	Leu	Leu	Lys	Thr	Val	Asp	Tyr	Trp	Ile	165	170	175	
Glu	Ile	Lys	Asp	Ala	Leu	Ile	Gly	Lys	Glu	Asp	Lys	Val	Ile	Ile	Asn	180	185	190	
Ile	Ser	Asn	Glu	Trp	Phe	Gly	Ser	Trp	Ser	Ser	Glu	Gly	Trp	Ala	Asp	195	200	205	
Gly	Tyr	Lys	Lys	Ala	Ile	Pro	Leu	Leu	Arg	Glu	Ala	Gly	Leu	Lys	His	210	215	220	
Thr	Leu	Met	Val	Asp	Ala	Ala	Gly	Trp	Gly	Gln	Phe	Pro	Arg	Ser	Ile	225	230	235	240
His	Glu	Lys	Gly	Leu	Glu	Val	Phe	Asn	Ser	Asp	Pro	Leu	Lys	Asn	Thr	245	250	255	
Met	Phe	Ser	Ile	His	Met	Tyr	Glu	Trp	Ala	Ala	Gly	Asn	Pro	Gln	Gln	260	265	270	
Val	Lys	Asp	Asn	Ile	Asp	Gly	Val	Leu	Glu	Lys	Asn	Leu	Ala	Val	Val	275	280	285	
Ile	Gly	Glu	Phe	Gly	His	His	His	Tyr	Gly	Arg	Asp	Val	Ala	Val	Asp	290	295	300	

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 305 310 315 320

Ser Trp His Gly Asn Ser Gly Gly Val Glu Tyr Leu Asp Leu Ala Thr  
 325 330 335

Asp Phe Ser Gly Thr Gln Leu Thr Glu Trp Gly Glu Arg Ile Val His  
 340 345 350

Gly Pro Asn Gly Leu Lys Glu Thr Ser Glu Ile Val Ser Val Tyr Lys  
 355 360 365

Lys

<210> 17  
 <211> 915  
 <212> DNA  
 <213> Bacillus sp.

<400> 17  
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 cgcaatgtta tgttctccat acacatgtac ggttcctgga ataatacagtc gcgaatcggc 180  
 agcgaattgc aggccatcaa agaccttggt cttgctgtca tgattggtga attcggatac 240  
 aactacaaca acggcaataa caacttgggg agtcagggtta acgcccagga aatcatgaat 300  
 caggcgcaag caaaaggaat cggctacatg ccgtgggtcgt ggactggcaa tgacgcggct 360  
 aactcttggt tggatatgac aacaaacgat tggcaaacac ttacatcatg ggggaatcta 420  
 gttgtaaatg gaaccaacgg cattcgagct acgtctgtcc cagcaactgt atttaataca 480  
 caaacaacaa tttatgattt tgaaggcggc aatgcccagg gctggtcagg ttccggtttg 540  
 agcggggggc cttggtctgt taatgaatgg gcggcgagcg gtagttattc tctcaaagcg 600  
 aatataatctc taggcgccac tcaaaaagct ttgcaaacca cagcgtccca taatttcagc 660  
 ggccgggtcta cattatccgt aagagtaaag catgcagcat ggggaaatca cggcagcggt 720  
 atgcaagcca agttatatgt gaaaacaggg gccggttacg cctggtatga tggcggcact 780  
 gtaaacatca acagctcggg caacacattg acgctaacc tggcaggcat tcctaattcg 840  
 aacgacgtca gagaactcgg aattgaattt ataacacctg caaattcgag tggttctttc 900  
 gcaatttatg ttgac 915

<210> 18  
 <211> 305  
 <212> PRT  
 <213> Bacillus sp.

<400> 18  
 Ile Ser Thr Leu Arg Asn Ala Gly Ile Arg Asn Thr Ile Val Val Asp  
 1 5 10 15

Ala Ser Gly Trp Gly Gln Asn Ser Ser Pro Ile Lys Ala Tyr Gly Asn  
 20 25 30

Glu Val Leu Asn His Asp Pro Gln Arg Asn Val Met Phe Ser Ile His  
 35 40 45

Met Tyr Gly Ser Trp Asn Asn Gln Ser Arg Ile Gly Ser Glu Leu Gln  
 50 55 60

Ala Ile Lys Asp Leu Gly Leu Ala Val Met Ile Gly Glu Phe Gly Tyr

65

70

75

80

Asn Tyr Asn Asn Gly Asn Asn Asn Leu Gly Ser Gln Val Asn Ala Gln  
                     85                    90                    95  
 Glu Ile Met Asn Gln Ala Gln Ala Lys Gly Ile Gly Tyr Met Pro Trp  
                     100                    105                    110  
 Ser Trp Thr Gly Asn Asp Ala Ala Asn Ser Trp Leu Asp Met Thr Thr  
                     115                    120                    125  
 Asn Asp Trp Gln Thr Leu Thr Ser Trp Gly Asn Leu Val Val Asn Gly  
                     130                    135                    140  
 Thr Asn Gly Ile Arg Ala Thr Ser Val Pro Ala Thr Val Phe Asn Thr  
                     145                    150                    155                    160  
 Gln Thr Thr Ile Tyr Asp Phe Glu Gly Gly Asn Ala Gln Gly Trp Ser  
                     165                    170                    175  
 Gly Ser Gly Leu Ser Gly Gly Pro Trp Ser Val Asn Glu Trp Ala Ala  
                     180                    185                    190  
 Ser Gly Ser Tyr Ser Leu Lys Ala Asn Ile Ser Leu Gly Ala Thr Gln  
                     195                    200                    205  
 Lys Ala Leu Gln Thr Thr Ala Ser His Asn Phe Ser Gly Arg Ser Thr  
                     210                    215                    220  
 Leu Ser Val Arg Val Lys His Ala Ala Trp Gly Asn His Gly Ser Gly  
                     225                    230                    235                    240  
 Met Gln Ala Lys Leu Tyr Val Lys Thr Gly Ala Gly Tyr Ala Trp Tyr  
                     245                    250                    255  
 Asp Gly Gly Thr Val Asn Ile Asn Ser Ser Gly Asn Thr Leu Thr Leu  
                     260                    265                    270  
 Asn Leu Ala Gly Ile Pro Asn Leu Asn Asp Val Arg Glu Leu Gly Ile  
                     275                    280                    285  
 Glu Phe Ile Thr Pro Ala Asn Ser Ser Gly Ser Phe Ala Ile Tyr Val  
                     290                    295                    300

Asp  
 305

<210> 19  
 <211> 397  
 <212> DNA  
 <213> *Bacillus clausii*

<400> 19  
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 ggattggcgc aaactggatt tcaagtaaca gggaccagtg tgcttgatgg agaggggcaat 120  
 ccgtatgtga tgcgtggagt caatcacgga cattcatggt tcaaacaaga ccttgataca 180  
 gcaataccag ctattgcagc gactggcgct aatacgggtga gaatcgtttt atcgaatggc 240  
 caacaatggg agcgagatac cgtagcggaa gttgaaagag tgcttgacagt taccgaagag 300

gaaggcttga cggctgtact tgaagttcat gatgcgacgg gaagtgatga tccaaacgat 360  
 ttgtttactg cagtggagta ttggtcagag agaggat 397

<210> 20  
 <211> 132  
 <212> PRT  
 <213> *Bacillus clausii*

<400> 20  
 Ile Ser Gln Gly Leu Val Gly Val Ile Ile Leu Leu Tyr Met Ala Phe  
 1 5 10 15  
 Ser Gln Glu Arg Gly Leu Ala Gln Thr Gly Phe Gln Val Thr Gly Thr  
 20 25 30  
 Gln Leu Leu Asp Gly Glu Gly Asn Pro Tyr Val Met Arg Gly Val Asn  
 35 40 45  
 His Gly His Ser Trp Phe Lys Gln Asp Leu Asp Thr Ala Ile Pro Ala  
 50 55 60  
 Ile Ala Ala Thr Gly Ala Asn Thr Val Arg Ile Val Leu Ser Asn Gly  
 65 70 75 80  
 Gln Gln Trp Glu Arg Asp Thr Val Ala Glu Val Glu Arg Val Leu Ala  
 85 90 95  
 Val Thr Glu Glu Glu Gly Leu Thr Ala Val Leu Glu Val His Asp Ala  
 100 105 110  
 Thr Gly Ser Asp Asp Pro Asn Asp Leu Phe Thr Ala Val Glu Tyr Trp  
 115 120 125  
 Ser Glu Arg Gly  
 130

<210> 21  
 <211> 960  
 <212> DNA  
 <213> *Bacillus sp.*

<400> 21  
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 gacaaaaatg gcgatcctta cgttatgcgt ggcgtcaacc atggacattc ttggtttaaa 180  
 caagatttag aggaggcaat ccctgccata gcagaaacag gggcgaacac agtgagaatc 240  
 gtcttatcca atggacagca atgggaaaaa gatgatgcct ctgagcttgc cctgtgtgctt 300  
 gctgccacag aaacatatgg gttgacaacc gtgctggaag tccacgatgc tacaggaagt 360  
 gataatcccg atgatttaga taaagcagtc gattactgga tcgaaatggc tgatgttcta 420  
 aaggggacag aagaccgggt aatcattaac attgccaatg aatggtatgg ggcgtggagg 480  
 agtgacgttt gggcagaggc atacgcacaa gcgatccccg gcttgccgag tgctggcctc 540  
 gcccatcgt taatagttag tgcggcaggt tggggacagt accctgcctc tatccatgag 600  
 cggggagccg acgtatttgc ctccgatcca ttaaaaaaca caatgttttc catccatatg 660  
 tacgaatatg caggagcggg tagggcgaca gtttctgaaa acatcgacgg tgtacttgct 720  
 gaaaatcttg ctgtggtaat cgggtgaattt ggccataggg atcatgatgg cgatgtcgat 780  
 gaagatgcga ttttggccta tacagcagag cggcaagtgg gctggcttgc ctggtcatgg 840  
 tatggcaata gcgggggtgt tgaatacttg gatttaactg aaggcccatc aggtccatta 900

accgagttggg gcgaacggat tgtctatggg gaaatgggct taaaagtaat tgatcacttg 960

<210> 22  
 <211> 320  
 <212> PRT  
 <213> Bacillus sp.

<400> 22  
 Met Asn Arg Lys Arg Leu Gln Trp Val Gly Ala Leu Val Val Val Leu  
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 Val Leu Phe Val Tyr Ser Ser Gly Leu Ala Ser Ala Gln Ser Gly Phe  
           20                    25                    30  
 His Val Lys Gly Thr Glu Leu Leu Asp Lys Asn Gly Asp Pro Tyr Val  
           35                    40                    45  
 Met Arg Gly Val Asn His Gly His Ser Trp Phe Lys Gln Asp Leu Glu  
           50                    55                    60  
 Glu Ala Ile Pro Ala Ile Ala Glu Thr Gly Ala Asn Thr Val Arg Ile  
     65                    70                    75                    80  
 Val Leu Ser Asn Gly Gln Gln Trp Glu Lys Asp Asp Ala Ser Glu Leu  
                     85                    90                    95  
 Ala Arg Val Leu Ala Ala Thr Glu Thr Tyr Gly Leu Thr Thr Val Leu  
           100                    105                    110  
 Glu Val His Asp Ala Thr Gly Ser Asp Asn Pro Asp Asp Leu Asp Lys  
           115                    120                    125  
 Ala Val Asp Tyr Trp Ile Glu Met Ala Asp Val Leu Lys Gly Thr Glu  
           130                    135                    140  
 Asp Arg Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr Gly Ala Trp Arg  
     145                    150                    155                    160  
 Ser Asp Val Trp Ala Glu Ala Tyr Ala Gln Ala Ile Pro Arg Leu Arg  
           165                    170                    175  
 Ser Ala Gly Leu Ala His Thr Leu Ile Val Asp Ala Ala Gly Trp Gly  
           180                    185                    190  
 Gln Tyr Pro Ala Ser Ile His Glu Arg Gly Ala Asp Val Phe Ala Ser  
           195                    200                    205  
 Asp Pro Leu Lys Asn Thr Met Phe Ser Ile His Met Tyr Glu Tyr Ala  
           210                    215                    220  
 Gly Ala Asp Arg Ala Thr Val Ser Glu Asn Ile Asp Gly Val Leu Ala  
     225                    230                    235                    240  
 Glu Asn Leu Ala Val Val Ile Gly Glu Phe Gly His Arg His His Asp  
           245                    250                    255  
 Gly Asp Val Asp Glu Asp Ala Ile Leu Ala Tyr Thr Ala Glu Arg Gln  
           260                    265                    270

55429055155555

Val Gly Trp Leu Ala Trp Ser Trp Tyr Gly Asn Ser Gly Gly Val Glu  
275 280 285

Tyr Leu Asp Leu Thr Glu Gly Pro Ser Gly Pro Leu Thr Ser Trp Gly  
290 295 300

Glu Arg Ile Val Tyr Gly Glu Met Gly Leu Lys Val Ile Asp His Leu  
305 310 315 320

<210> 23  
<211> 564  
<212> DNA  
<213> Bacillus sp.

<400> 23  
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gacaaaaatg gcgatcctta cgttatgcgt ggcgtcaacc atggacattc ttggtttaaa 180  
caagatttag aggaggcaat ccctgccata gcagaaacag gggcgaacac agtgagaatc 240  
gtcttatcca atggacagca atgggaaaaa gatgatgcct ctgagcttgc ccgtgtgctt 300  
gctgccacag aaacatatgg gttgacaacc gtgctggaag tccacgatgc tacaggaagt 360  
gataatcccg atgatttaga taaagcagtc gattactgga tcgaaatggc tgatgttcta 420  
aaggggacag aagaccgggt aatcattaac attgccaatg aatgggtatgg ggcgtggagg 480  
agtgaccttt gggcaaaagc atacgcacaa gcgatccgc gcttgccgag tgctggcctc 540  
gcccatacgt taataattga tgcc 564

<210> 24  
<211> 188  
<212> PRT  
<213> Bacillus sp.

<400> 24  
Met Asn Arg Lys Arg Leu Gln Trp Val Gly Ala Leu Val Ala Val Leu  
1 5 10 15

Val Leu Phe Val Tyr Ser Ser Gly Leu Ala Ser Ala Gln Ser Gly Phe  
20 25 30

His Val Lys Gly Thr Glu Leu Leu Asp Lys Asn Gly Asp Pro Tyr Val  
35 40 45

Met Arg Gly Val Asn His Gly His Ser Trp Phe Lys Gln Asp Leu Glu  
50 55 60

Glu Ala Ile Pro Ala Ile Ala Glu Thr Gly Ala Asn Thr Val Arg Ile  
65 70 75 80

Val Leu Ser Asn Gly Gln Gln Trp Glu Lys Asp Asp Ala Ser Glu Leu  
85 90 95

Ala Arg Val Leu Ala Ala Thr Glu Thr Tyr Gly Leu Thr Thr Val Leu  
100 105 110

Glu Val His Asp Ala Thr Gly Ser Asp Asn Pro Asp Asp Leu Asp Lys

554290:554290

115

120

125

Ala Val Asp Tyr Trp Ile Glu Met Ala Asp Val Leu Lys Gly Thr Glu  
130 135 140

Asp Arg Val Ile Ile Asn Ile Ala Asn Glu Trp Tyr Gly Ala Trp Arg  
145 150 155 160

Ser Asp Leu Trp Ala Lys Ala Tyr Ala Gln Ala Ile Pro Arg Leu Arg  
165 170 175

Ser Ala Gly Leu Ala His Thr Leu Ile Ile Asp Ala  
180 185

&lt;210&gt; 25

&lt;211&gt; 2445

&lt;212&gt; DNA

&lt;213&gt; Bacillus sp.

&lt;400&gt; 25

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caaagcctac cttactatgt gaacgctatc aatgaaggcg agagagaagc ttttgcaccc 120  
gcagggagat atgatgctga acaggcgact acgacaggaa atgccgtatt cacgaccgag 180  
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ttatctatcg gatactatgc tccatacggg aacaagggaa ccacaattct ggtgaacggt 360  
gcaggtaacg gagagtttat gttgccagcg cccgaggacg gggcagtcct cgcggaagt 420  
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tttattgaag cagaagaaga ttacgaagcg actggaaatg ttagcggttac caatgaaatc 600  
gaaggttatt ccggagcagg ctatttggtc aaccaagagg ggacaattca ttggaatgta 660  
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gacttgagaa	tcggttatgg	ggacgtctgg	atcgtcatcc	cacacgaaca	gcttgggggt	2400
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<210> 26
<211> 815
<212> PRT
<213> Bacillus sp.
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<400> 26
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Val Phe Met Phe Gln Ser Leu Pro Tyr Tyr Val Asn Ala Ile Asn Glu
                20                      25                      30
Gly Glu Arg Gln Ala Phe Ala Ser Ala Gly Arg Tyr Asp Ala Glu Gln
                35                      40                      45
Ala Thr Thr Thr Gly Asn Ala Val Phe Thr Thr Glu Pro Val Glu Asp
  50                      55                      60
Gly Glu Tyr Ala Gly Pro Gly Tyr Ile Ser Phe Phe Ser Glu Asp Ser
  65                      70                      75                      80
Ser Pro Pro Ser Ser Ser Thr Thr Phe His Ile Gln Ala Asp Lys Thr
                85                      90                      95
Glu Leu Tyr His Leu Ser Ile Gly Tyr Tyr Ala Pro Tyr Gly Asn Lys
                100                      105                      110
Gly Thr Thr Ile Leu Val Asn Gly Ala Gly Asn Gly Glu Phe Met Leu
                115                      120                      125
Pro Ala Pro Glu Asp Gly Ala Val Ser Ala Glu Val Glu Ile Ser Lys
  130                      135                      140
Ile Leu Leu Glu Glu Gly Asn Asn Thr Ile Thr Phe Thr Arg Gly Trp
  145                      150                      155                      160
Gly Tyr Tyr Gly Ile Glu Tyr Ile Arg Val Glu Pro Val Asn Pro Thr
                165                      170                      175
Leu Pro Thr Ile Phe Ile Glu Ala Glu Glu Asp Tyr Glu Ala Thr Gly
                180                      185                      190
Asn Val Ser Val Thr Asn Glu Ile Glu Gly Tyr Ser Gly Ala Gly Tyr
  195                      200                      205
Leu Phe Asn Gln Glu Gly Thr Ile His Trp Asn Val Thr Ser Pro Glu
  210                      215                      220
Thr Ser Ile Tyr Glu Val Ile Val Ala Tyr Ala Ala Pro Tyr Gly Asp
  225                      230                      235                      240
Lys Gln Thr Asn Leu Thr Val Asn Gly Gln Gly Thr Val Asn Leu Asp
                245                      250                      255
Leu Lys Glu Thr Glu Val Phe Val Glu Leu Asn Val Gly Ile Val Ser

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260	265	270
Leu Asn Glu Gly Glu Asn Thr 275	Leu Thr Leu His Ser 280	Gly Trp Gly Trp 285
Tyr Asn Ile Asp Tyr Ile Lys 290	Leu Val Pro Val Val 295	Ser Ser Asp Pro 300
Glu Pro His Gln Val Glu Lys Thr 305	Leu Val Asn Pro Asp 310	Ala Ser Pro 315
Glu Ala Arg Ala Leu Ile Asn Tyr 325	Leu Val Asp Gln Tyr 330	Gly Asn Lys 335
Ile Leu Ser Gly Gln Thr Glu 340	Leu Lys Asp Ala Arg 345	Trp Ile His Glu 350
Gln Val Gly Lys Tyr Pro Ala 355	Val Met Ala Val Asp 360	Phe Met Asp Tyr 365
Ser Pro Ser Arg Val Val His 370	Gly Ala Thr Gly Thr 375	Ala Val Glu Glu 380
Ala Ile Glu Trp Ala Glu Met Gly 385	Gly Gly Ile Ile Thr 390	Phe His Trp His 395
Trp Asn Ala Pro Lys Asp Leu 405	Leu Asn Val Pro Gly 410	Asn Glu Trp Trp 415
Ser Gly Phe Tyr Thr Arg Ala 420	Thr Thr Phe Asp Val 425	Glu Tyr Ala Leu 430
Glu Asn Arg Glu Ser Glu Asp 435	Phe Gln Leu Leu Ile 440	Ser Asp Met Asp 445
Val Ile Ala Glu Gln Leu Lys 450	Arg Leu Gln Ala Glu 455	Asn Ile Pro Val 460
Leu Trp Arg Pro Leu His Glu 465	Ala Glu Gly Gly Trp 470	Phe Trp Trp Gly 475
Ala Lys Gly Pro Glu Ala Ala 485	Ile Glu Leu Tyr Arg 490	Leu Met Tyr Asp 495
Arg Tyr Thr Asn His His Lys 500	Leu Asn Asn Leu Ile 505	Trp Met Trp Asn 510
Ser Glu Ala Glu Glu Trp Tyr 515	Pro Gly Asp Asp Val 520	Val Asp Met Ile 525
Ser Thr Asp Ile Tyr Asn Pro 530	Val Gly Asp Phe Ser 535	Pro Ser Ile Asn 540
Lys Tyr Glu His Leu Lys Glu 545	Leu Val Gln Asp Lys 550	Lys Leu Val Ala 555
Leu Pro Glu Thr Gly Ile Ile 565	Pro Asp Pro Asp Gln 570	Leu Gln Leu Phe 575
Asn Ala Asn Trp Ser Trp Phe 580	Ala Thr Trp Thr Gly 585	Asp Tyr Ile Arg 590

540 545 550 555 560 565 570 575 580 585 590

580

585

590

Asp Gly Ile Ser Asn Pro Ile Glu His Leu Gln Lys Val Phe His His  
595 600 605

Asp Tyr Val Ile Thr Leu Asp Glu Leu Pro Glu Asn Leu Ser Arg Tyr  
610 615 620

Gly Leu Ser Glu Gly Val Trp Lys Ser Asp Ala Asp Leu Ser Val Lys  
625 630 635 640

Thr Arg Thr Thr Ser Glu Ile Thr Val Asn Trp Ser Asn Ala Ile Gln  
645 650 655

Tyr Asp Ser Val Asn Gly Tyr Lys Leu Ile Lys Asp Gly Val Glu Thr  
660 665 670

Val Ser Val Glu Gly Gly Val Gln Glu Tyr Thr Phe Thr Asn Leu Leu  
675 680 685

Pro Gly Thr Gln Tyr Thr Ile Lys Val Glu Ala Leu Asp Gln Asp Asp  
690 695 700

Arg Trp Thr Ala Asp Gly Pro Val Ala Val Val Ser Thr Leu Ser Asn  
705 710 715 720

Ala Pro Ile Ser Tyr Pro Pro Ala Val Thr Pro Asp Glu Pro Asn Glu  
725 730 735

Glu Leu Ser Glu Gly Glu Tyr Thr Leu Leu Ala Asp Asp Leu Ser Ser  
740 745 750

Gln Asp Gly Val Leu Glu Val Ser Leu Glu Pro Thr Val Thr Lys Leu  
755 760 765

Ile Ile Pro Ser Ala Leu Ala Gly Thr Leu Asp Gly Asp Leu Arg Ile  
770 775 780

Gly Tyr Gly Asp Val Trp Ile Val Ile Pro His Glu Gln Leu Gly Gly  
785 790 795 800

Asp Glu Gln Gln Ser Gly Ser Ala Tyr Glu Leu Val Leu Glu Ile  
805 810 815

<210> 27

<211> 1488

<212> DNA

<213> Bacillus sp.

<400> 27

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gtaagaatat ttgaagctga agatgctatt ttaaatgggc tgactattaa aaattctgaa 180  
ccaggttttt ctggtaccgg atatgtaggt gactttgaaa atagctctca gagtgtgacg 240  
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tatggaagtg gaaaagtagc taatgttatt gtaaattggag agaagctaag tacttttaca 360  
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caacatgatt atccaaatac acgaccacga gatttagaat atatttatga aactactggg 660
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agcgaagagc acctaagaaa agtatataat catgattatg tgattaccct aaataaatta 1440
cctaacctta aaacatatag gggaagatgc acttatacag acactatc 1488

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<210> 28  
 <211> 496  
 <212> PRT  
 <213> Bacillus sp.

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 Asn Ile Ala Asn Ala Glu Ser Glu Val Arg Ile Phe Glu Ala Glu Asp  
 35 40 45  
 Ala Ile Leu Asn Gly Leu Thr Ile Lys Asn Ser Glu Pro Gly Phe Ser  
 50 55 60  
 Gly Thr Gly Tyr Val Gly Asp Phe Glu Asn Ser Ser Gln Ser Val Thr  
 65 70 75 80  
 Phe Gln Ile Glu Ala Pro Lys Ala Gly Leu Tyr Asn Leu Asn Ile Gly  
 85 90 95  
 Tyr Gly Ala Ile Tyr Gly Ser Gly Lys Val Ala Asn Val Ile Val Asn  
 100 105 110  
 Gly Glu Lys Leu Ser Thr Phe Thr Met Gly Ser Gly Phe Gly Lys Ala  
 115 120 125  
 Ser Ala Gly Lys Val Leu Leu Asn Ser Gly Leu Asn Thr Ile Ser Ile  
 130 135 140  
 Thr Pro Asn Trp Thr Trp Phe Thr Ile Asp Tyr Ile Glu Val Ile His  
 145 150 155 160  
 Ala Pro Glu Pro Glu Asn His Asn Val Glu Lys Thr Leu Ile Asn Pro  
 165 170 175  
 Asn Ala Thr Asp Glu Ala Lys Ala Leu Ile Ser Tyr Leu Val Asp Asn  
 180 185 190

Phe Gly Glu Lys Ile Leu Ala Gly Gln His Asp Tyr Pro Asn Thr Arg  
 195 200 205  
 Pro Arg Asp Leu Glu Tyr Ile Tyr Glu Thr Thr Gly Lys Tyr Pro Ala  
 210 215 220  
 Val Leu Gly Leu Asp Phe Ile Asp Asn Ser Pro Ser Arg Val Glu Arg  
 225 230 235 240  
 Gly Ala Ser Ala Asp Glu Thr Pro Val Ala Ile Asp Trp Trp Asn Lys  
 245 250 255  
 Gly Gly Ile Val Thr Phe Thr Trp His Trp Asn Ala Pro Lys Asp Leu  
 260 265 270  
 Leu Asp Glu Pro Gly Asn Glu Trp Trp Ser Gly Phe Tyr Thr Arg Ala  
 275 280 285  
 Thr Thr Phe Asp Val Glu Tyr Ala Leu Lys His Pro Lys Ser Glu Asp  
 290 295 300  
 Tyr Met Leu Leu Ile Arg Asp Ile Asp Val Ile Ala Gly Glu Leu Lys  
 305 310 315 320  
 Lys Leu Gln Glu Ala Asn Val Pro Val Leu Trp Arg Pro Leu His Glu  
 325 330 335  
 Ala Glu Gly Gly Trp Phe Trp Trp Gly Ala Lys Gly Pro Glu Ser Thr  
 340 345 350  
 Lys Glu Leu Trp Arg Leu Met Tyr Asp Arg Met Thr Asn Tyr His Asn  
 355 360 365  
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 370 375 380  
 Pro Gly Asp Glu Tyr Val Asp Ile Val Ser Phe Asp Ser Tyr Pro Gly  
 385 390 395 400  
 Glu Tyr Asn Tyr Ser Pro Met Ser Arg Glu Tyr Glu Ala Leu Lys Glu  
 405 410 415  
 Leu Ser Ser Asn Lys Lys Leu Ile Ala Ile Ala Glu Asn Gly Pro Ile  
 420 425 430  
 Pro Asp Pro Asp Leu Leu Gln Leu Tyr His Ala Asn Tyr Ser Trp Phe  
 435 440 445  
 Ala Thr Trp Asn Gly Asp Ile Leu Arg Asn Gln Asn Ser Glu Glu His  
 450 455 460  
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 465 470 475 480  
 Pro Asn Leu Lys Thr Tyr Arg Gly Arg Cys Thr Tyr Thr Asp Thr Ile  
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<210> 29  
 <211> 1086  
 <212> DNA  
 <213> *Bacillus licheniformis*

<400> 29  
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 gagctgatga attggcttgc tcatctgccg aaccgatcgg aaaatcgctg actgtcaggt 180  
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<210> 30  
 <211> 361  
 <212> PRT  
 <213> *Bacillus licheniformis*

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 Gln Asn Ala Gln Ser Thr Thr Lys Glu Leu Met Asn Trp Leu Ala His  
 35 40 45  
 Leu Pro Asn Arg Ser Glu Asn Arg Val Leu Ser Gly Ala Phe Gly Gly  
 50 55 60  
 Tyr Ser Asn Ala Thr Phe Ser Met Lys Glu Ala Asn Arg Ile Lys Asp  
 65 70 75 80  
 Ala Thr Gly Gln Ser Pro Val Val Tyr Ala Cys Asp Tyr Ser Arg Gly  
 85 90 95  
 Trp Leu Glu Thr Ala His Ile Ala Asp Ala Ile Asp Tyr Ser Cys Asn  
 100 105 110  
 Ser Asp Leu Ile Ser His Trp Lys Ser Gly Gly Ile Pro Gln Ile Ser  
 115 120 125

Met His Leu Pro Asn Pro Ala Phe Gln Ser Gly Asn Tyr Lys Thr Lys  
 130 135 140

Ile Ser Asn Ser Gln Tyr Glu Lys Ile Leu Asp Ser Ser Thr Thr Glu  
 145 150 155 160

Gly Lys Arg Leu Asp Ala Val Leu Ser Lys Val Ala Asp Gly Leu Gln  
 165 170 175

Gln Leu Lys Asn Glu Gly Val Pro Val Leu Phe Arg Pro Leu His Glu  
 180 185 190

Met Asn Gly Glu Trp Phe Trp Trp Gly Leu Thr Gly Tyr Asn Gln Lys  
 195 200 205

Asp Ser Glu Arg Ile Ser Leu Tyr Lys Gln Leu Tyr Gln Lys Ile Tyr  
 210 215 220

His Tyr Met Thr Asp Thr Arg Gly Leu Asp Asn Leu Ile Trp Val Tyr  
 225 230 235 240

Ala Pro Asp Ala Asn Arg Asp Phe Lys Thr Asp Phe Tyr Pro Gly Asp  
 245 250 255

Ser Tyr Val Asp Ile Val Gly Leu Asp Ala Tyr Phe Ser Asp Ala Tyr  
 260 265 270

Ser Ile Lys Gly Tyr Asp Glu Leu Thr Ala Leu Asn Lys Pro Phe Ala  
 275 280 285

Phe Thr Glu Val Gly Pro Gln Thr Thr Asn Gly Ser Leu Asp Tyr Ser  
 290 295 300

Gln Phe Ile Asn Ala Val Lys Gln Lys Tyr Pro Lys Thr Ile Tyr Phe  
 305 310 315 320

Leu Ala Trp Asp Glu Gly Trp Ser Pro Ala Ala Asn Gln Gly Ala Phe  
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Asn Leu Tyr Asn Asp Ser Trp Thr Leu Asn Lys Gly Glu Leu Trp Glu  
 340 345 350

Gly Ser Ser Leu Thr Pro Ala Ala Glu  
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<210> 31

<211> 3041

<212> DNA

<213> Caldocellulosiruptor sp.

<400> 31

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 aatgtatcaa aaaggtgtca gtttctactg atttgcagcg acctggtaac aagtatgcgc 420

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&lt;210&gt; 32

&lt;211&gt; 903

&lt;212&gt; PRT

<213> *Caldocellulosiruptor* sp.

&lt;400&gt; 32

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Leu Leu Gly Leu Leu Pro Thr Gly Ile Phe Gly Ala Val Glu Thr Ser
      20             25             30

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Val Gln Ser Tyr Val Phe Asp Phe Glu Asp Gly Thr Thr Met Thr Phe
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Gly Glu Ala Trp Gly Asp Ser Leu Lys Cys Ile Lys Lys Val Ser Val  
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 Ser Thr Asp Leu Gln Arg Pro Gly Asn Lys Tyr Ala Leu Arg Leu Asp  
 65 70 75 80  
 Val Glu Phe Asn Glu Asn Asn Gly Trp Asp Gln Gly Asp Leu Gly Ala  
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 Trp Ile Gly Gly Val Val Glu Gly Gln Phe Asp Phe Thr Asn Tyr Lys  
 100 105 110  
 Ser Val Glu Phe Glu Met Phe Val Pro Tyr Asp Glu Phe Ala Lys Ala  
 115 120 125  
 Lys Gly Gly Phe Ala Tyr Lys Val Val Leu Asn Asp Gly Trp Lys Glu  
 130 135 140  
 Leu Gly Ser Glu Phe Ser Ile Thr Val Asn Ala Gly Lys Lys Val Lys  
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 Asp Asp Phe Arg Thr Lys Lys Arg Ala Gln Leu Val Phe Gln Phe Ala  
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 Lys Ile Ile Lys Asp Phe Thr Leu Leu Asn Tyr Lys Asp Lys Thr Thr  
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Trp Lys Glu Ile Asn Gly Lys Thr Tyr Ala Val Ile Lys Cys Lys Asp  
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 Ala Gly Ser Tyr Val Lys Tyr Thr Gly Pro Ile Tyr Ile Asp Asn Val  
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 Thr Leu Ile Ala Gly Lys Lys Val Ala Pro Lys Val Glu Arg Ile Ser  
 420 425 430  
 Leu Pro Asn Pro Lys Thr Tyr Tyr Lys Val Lys Ile Glu Ala Glu Ser  
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 Ala Ser Asp Gly Trp Ala Tyr Ser Val Glu Lys Glu Asn Ala Lys Phe  
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 Ser Gly Lys Gly Tyr Val Leu Leu Phe Gly Asn Asn Met Gly Asn Thr  
 465 470 475 480  
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 515 520 525  
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 530 535 540  
 Glu His Thr Ile Ser Leu Gln Lys Ser Gly Gly Tyr Thr Ile Ala Val  
 545 550 555 560  
 Asp Tyr Phe Val Ile Glu Glu Leu Val Ala Ala Asn Lys Ser Lys Leu  
 565 570 575  
 Ser Val Ser Ser Lys Leu Val Thr Pro Asn Pro His Pro Asn Ala Gln  
 580 585 590  
 Arg Leu Ile Asn Tyr Leu Ser Ser Ile Tyr Gly Glu Lys Ile Leu Ser  
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 Val Thr Lys Arg Tyr Pro Ala Val Arg Ser Phe Asp Phe Met Asp Tyr  
 625 630 635 640  
 Ser Pro Ser Arg Val Gln His Gly Thr Lys Gly Thr Asp Val Asp Glu  
 645 650 655  
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 660 665 670  
 Trp Asn Ala Pro Thr Gly Leu Ile Asp Gln Pro Gly Lys Glu Trp Trp  
 675 680 685

Arg Gly Phe Tyr Thr Glu Ala Thr Thr Phe Asp Leu Lys Lys Ala Met  
690 695 700

Asp Asn Pro Asn Ser Glu Glu Tyr Lys Leu Ile Leu Arg Asp Ile Asp  
705 710 715 720

Ala Ile Ala Glu Gln Leu Lys Lys Leu Gln Ala Glu Gly Val Pro Val  
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Leu Phe Arg Pro Leu His Glu Ala Ser Gly Gly Trp Phe Trp Trp Gly  
740 745 750

Ala Lys Gly Pro Glu Pro Tyr Ile Lys Leu Trp Lys Leu Met Phe Asp  
755 760 765

Arg Leu Val Asn Tyr His Lys Ile Asn Asn Leu Ile Trp Val Trp Asn  
770 775 780

Gly Gln Asp Ala Ala Trp Tyr Pro Gly Asp Gln Tyr Val Asp Ile Ile  
785 790 795 800

Ala Glu Asp Ile Tyr Glu Glu Lys Ala Gln Tyr Ser Pro Tyr Thr Glu  
805 810 815

Arg Phe Val Lys Ala Leu Lys Tyr Thr Asn Ala Asn Lys Met Ile Ala  
820 825 830

Leu Ser Glu Cys Gly Thr Ile Pro Asp Pro Ala Val Leu Lys Gln Glu  
835 840 845

Gly Val Ser Trp Leu Trp Phe Ser Val Trp Ala Gly Ser Tyr Val Met  
850 855 860

Thr Gly Ser Lys Tyr Asn Asp Glu Trp Asn Asp Asn His Met Leu Arg  
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Ile Lys Ser Ile Pro Leu Lys  
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<210> 33

<211> 1450

<212> RNA

<213> Bacillus sp. I633

<400> 33

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&lt;210&gt; 34

&lt;211&gt; 1508

&lt;212&gt; RNA

&lt;213&gt; Bacillus sp. AAI12

&lt;400&gt; 34

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gaaggugc						1508